

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.

(ii) TITLE OF THE INVENTION: A NOVEL PROSTATE-ASSOCIATED
KALLIKREIN

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0195 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Trp	Phe	Leu	Val	Leu	Cys	Leu	Ala	Leu	Ser	Leu	Gly	Gly	Thr	Gly	1	5	10	15
Ala	Ala	Pro	Pro	Ile	Gln	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu	Cys	Glu	20	25	30	
Gln	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Tyr	His	Phe	Ser	Thr	Phe	35	40	45	
Gln	Cys	Gly	Gly	Ile	Leu	Val	His	Arg	Gln	Trp	Val	Leu	Thr	Ala	Ala	50	55	60	
His	Cys	Ile	Ser	Asp	Asn	Tyr	Gln	Leu	Trp	Leu	Gly	Arg	His	Asn	Leu	65	70	75	80
Phe	Asp	Asp	Glu	Asn	Thr	Ala	Gln	Phe	Val	His	Val	Ser	Glu	Ser	Phe	85	90	95	

Pro His Pro Gly Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
 100 105 110
 Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
 115 120 125
 Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
 130 135 140
 Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
 145 150 155 160
 Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
 165 170 175
 Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys
 180 185 190
 Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
 195 200 205
 Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
 210 215 220
 Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
 225 230 235 240
 Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
 245 250 255
 Thr Ile Ala Glu Asn Ser
 260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTGGCCCT	GGACACCTCT	GTCACCATGT	GGTTCCTGGT	TCTGTGCCTC	GCCCTGTCCC	60
TGGGGGGGAC	TGGTGCTGCG	CCCCCGATTG	AGTCCCGGAT	TGTGGGAGGC	TGGGAGTGTG	120
AGCAGCATTC	CCAGCCCTGG	CAGGCGGCTC	TGTACCAGAA	GACGCGGCTA	CTCTGTGGGG	180
CGACGNTCAT	NGCCCCCAGA	TGGTTCCTGA	CAGCAGCCCA	CTGCCTNAAG	CCCCGCTACA	240
TAGTTCACCT	GGGGCAGCAC	AACCTCCAGA	AGGAGGAGGG	CTGTGAGCAG	ACCCGGACAG	300
CCACTGAGTC	CTTCCCCCAC	CCCGGCTTCA	ACAACAGCCT	CCCCAACAAA	GACCACCGCA	360
ATGACATCAT	GCTGGTGAAG	ATGGCATCGC	CAGTCTCCAT	CACCTGGGCT	GTGCGACCCC	420
TCACCCTCTC	CTCACGCTGT	GTCACGTGCTG	GCACCAGCTG	CCTCATTTCC	GGCTGGGGCA	480
GCACGTCCAG	CCCCCAGTTA	CGCCTGCCTC	ACACCTTGCG	ATGCGCCAAC	ATCACCATCA	540
TTGAGCACCA	GAAGTGTGAG	AACGCCTACC	CCGGCAACAT	CACAGACACC	ATGGTGTGTG	600
CCAGCGTGCA	GGAAGGGGGC	AAGGACTCCT	GCCAGGGTGA	CTCCGGGGGC	CCTCTGGTCT	660
GTAACCAAGTC	TCTTCAAGGC	ATTATCTCCT	GGGGCCAGGA	TCCGTGTGCG	ATCACCCGAA	720
AGCCTGGTGT	CTACACGAAA	GTCTGCAAA	ATGTGGACTG	GATCCAGGAG	ACGATGAAGA	780
ACAATTAGAC	TGGACNTCAC	CTCCGAANCC	CCCACAGCCC	ATCACCTCC	ATT	833

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 186653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
 1 5 10 15
 Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
 20 25 30
 Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
 35 40 45

Gln Cys Gly Gl e Leu Val His Arg Gln Trp Val Thr Ala Ala
 50 55 60
 His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
 65 70 75 80
 Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
 85 90 95
 Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
 100 105 110
 Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
 115 120 125
 Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
 130 135 140
 Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
 145 150 155 160
 Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
 165 170 175
 Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys
 180 185 190
 Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
 195 200 205
 Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
 210 215 220
 Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
 225 230 235 240
 Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
 245 250 255
 Thr Ile Ala Glu Asn Ser
 260

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 55527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Trp Phe Leu Ile Leu Phe Leu Ala Leu Phe Leu Gly Gly Ile Asp
 1 5 10 15
 Ala Ala Pro Pro Val Gln Ser Arg Ile Ile Gly Gly Phe Asn Cys Glu
 20 25 30
 Lys Asn Ser Gln Pro Trp His Val Ala Val Tyr Arg Phe Ala Arg Tyr
 35 40 45
 Gln Cys Gly Gly Val Leu Leu Asp Ala Asn Trp Val Leu Thr Ala Ala
 50 55 60
 His Cys Tyr Asn Asp Lys Tyr Gln Val Trp Leu Gly Lys Asn Asn Arg
 65 70 75 80
 Phe Glu Asp Glu Pro Ser Ala Gln His Gln Leu Ile Ser Lys Ala Ile
 85 90 95
 Pro His Pro Gly Phe Asn Met Ser Leu Leu Asn Lys Asp His Thr Pro
 100 105 110
 His Pro Glu Asp Asp Tyr Ser Asn Asp Leu Met Leu Val Arg Leu Lys
 115 120 125
 Lys Pro Ala Glu Ile Thr Asp Val Val Lys Pro Ile Asp Leu Pro Thr
 130 135 140
 Glu Glu Pro Thr Val Gly Ser Arg Cys Leu Ala Ser Gly Trp Gly Ser
 145 150 155 160
 Thr Thr Pro Thr Glu Glu Phe Glu Tyr Ser His Asp Leu Gln Cys Val
 165 170 175
 Tyr Leu Glu Leu Ser Asn Glu Val Cys Ala Lys Ala His Thr Glu
 180 185 190
 Lys Val Thr Asp Thr Met Leu Cys Ala Gly Glu Met Asp Gly Gly Lys
 195 200 205

